



Release 2.1D John F. Collins, Biocomputing Research Unit.
Copyright (c) 1993, 1994, 1995 University of Edinburgh, U.K.
Distribution rights by Intelligentics, Inc.

Msrch_un n.a. - n.a. database search, using Smith-Waterman algorithm

on: Thu Aug 21 10:35:24 1997; Maspar time 451.64 Seconds
929.139 Million cell updates/sec

Tabular output not generated.

Title: >US-08-469-637A-1
Description: (1-1527) from US08469637A.seq
Perfect Score: 1527
N.A. Sequence: 1 GCCCCAGCGCGCGCTCCAA.....TTCACCTGAGAAAAA 1527
Comp: GCGGGCTCGCGCGGAGGT.....AAGTTGACCTTTTTTTT

Scoring table: TABLE default

Gap 6

Rmatch STD : Dbase 0; Query 0

Searched: 359085 seqs, 137405154 bases x 2

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: EST-STS-THREE
1:EST199 2:EST200 3:EST201 4:EST202 5:EST203 6:EST204
7:EST205 8:EST206 9:EST207 10:EST208 11:EST209 12:EST210
13:EST211 14:EST212 15:EST213 16:EST214 17:EST215
18:EST216 19:EST217 20:EST218 21:EST219 22:EST220
23:EST221 24:EST222 25:EST223 26:EST224 27:EST225
28:EST226 29:EST227 30:EST228 31:EST229 32:EST230
33:EST231 34:EST232 35:EST233 36:STS1 37:STS2 38:STS3
39:STS4 40:STS5 41:STS6 42:STS7 43:STS8 44:STS9 45:STS10
46:STS11 47:STS12 48:STS13
EST-STS-FOUR
49:ESTST1 50:ESTST2 51:ESTST3 52:ESTST4 53:ESTST5
54:ESTST6 55:ESTST7 56:ESTST8 57:ESTST9 58:ESTST10
59:ESTST11 60:ESTST12 61:ESTST13 62:ESTST14 63:ESTST15
64:ESTST16 65:ESTST17 66:ESTST18 67:ESTST19 68:ESTST20
69:ESTST21 70:ESTST22 71:ESTST23 72:ESTST24 73:ESTST25
74:ESTST26 75:ESTST27 76:ESTST28 77:ESTST29 78:ESTST30
79:ESTST31 80:ESTST32 81:ESTST33 82:ESTST34 83:ESTST35
84:ESTST36 85:ESTST37 86:ESTST38 87:ESTST39 88:ESTST40
89:ESTST41 90:ESTST42 91:ESTST43 92:ESTST44 93:ESTST45
94:ESTST46 95:ESTST47 96:ESTST48 97:ESTST49 98:ESTST50
99:ESTST51 100:ESTST52 101:ESTST53 102:ESTST54
103:ESTST55 104:ESTST56 105:ESTST57 106:ESTST58 107:ESTST59
108:ESTST60

Statistics: Mean 11.492; Variance 1.942; scale 5.918
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result Query

SUMMARIES

No.	Score	Match	Length	DB	ID	Description	Pred. No.
1	461	30.2	463	65	AA233719	z17908.r1 Soares NIH	0.00e+00
2	461	30.2	463	83	HS1151638	z17908.r1 Soares NIH	0.00e+00
3	335	21.9	530	16	AA195113	z135a03.r1 Soares NIH	0.00e+00
4	335	21.9	530	54	AA195113	z135a03.r1 Soares NIH	0.00e+00
5	21	1.4	105	91	KM1135	mp42d03.r1 Soares mou	9.46e-03
6	21	1.4	107	98	NMAA17046	mp33f02.r1 Soares 2nb	9.46e-03
7	21	1.4	107	5	AA117046	mp33f02.r1 Soares 2nb	9.46e-03
8	21	1.4	156	36	DM36D75	D. melanogaster STS d	9.46e-03
9	21	1.4	194	48	HOMUT5145	Human STS UT5145.	9.46e-03
10	21	1.4	212	12	AA181616	zps2d02.r1 Stratagene	9.46e-03
11	22	1.4	241	77	AT48713	15616 Arabidopsis th	5.47e-04
12	22	1.4	245	40	G11923	human STS MR4116	9.46e-03
13	21	1.4	253	38	G06067	human STS WT-6405.	9.46e-03
14	22	1.4	267	95	NM5835	ma38f10.r1 Soares mou	5.47e-04
15	22	1.4	281	92	NM1157384	mv25d08.r1 GuayWoodto	5.47e-04
16	22	1.4	312	42	AA239461	human STS WT-1391	9.46e-03
17	21	1.4	343	59	AA124222	mp8c08.r1 Soares 2nb	5.47e-04
18	22	1.4	343	7	AA124222	mp8c08.r1 Soares 2nb	5.47e-04
19	22	1.4	351	36	DM122E45	D. melanogaster STS d	9.46e-03
20	21	1.4	377	90	NM05110	mb39g02.r1 Soares mou	9.46e-03
21	21	1.4	380	60	AA142684	mg64e05.r1 Soares 2nb	9.46e-03
22	21	1.4	380	100	NMAA42684	mg64e05.r1 Soares 2nb	9.46e-03
23	21	1.4	392	53	T03759	IB862 Infant Brain, B	9.46e-03
24	25	21	400	39	G10922	human STS SHCG-13782	5.47e-04
25	22	1.4	412	70	AA222925	mv98c06.r1 GuayWoodto	9.46e-03
26	22	1.4	422	67	AA241200	mp85h10.r1 Soares mou	9.46e-03
27	21	1.4	427	76	AT3618	zps7h05.r1 Stratagene	9.46e-03
28	21	1.4	427	76	AT3618	zps7h05.r1 Stratagene	9.46e-03
29	21	1.4	427	76	AT3618	zps7h05.r1 Stratagene	9.46e-03
30	21	1.4	427	76	AT3618	zps7h05.r1 Stratagene	9.46e-03
31	21	1.4	431	21	AA219045	zq16e09.r1 Stratagene	9.46e-03
32	21	1.4	439	21	AA020160	mh49h05.r1 Soares mou	9.46e-03
33	21	1.4	443	60	AA213094	mw82b02.r1 Soares mou	9.46e-03
34	21	1.4	443	22	AA213094	mw82b02.r1 Soares mou	9.46e-03
35	21	1.4	443	98	NMAA13451	mw82b02.r1 Soares mou	9.46e-03
36	22	1.4	450	48	HOMUT1054	Human STS UT1054.	5.47e-04
37	21	1.4	457	99	NMAA25146	mp78f05.r1 Soares 2nb	9.46e-03
38	21	1.4	457	60	AA125146	mp78f05.r1 Soares 2nb	9.46e-03
39	22	1.4	472	77	AT4774	5740 Arabidopsis th1	5.47e-04
40	21	1.4	496	76	AT35319	21953 Arabidopsis th	9.46e-03
41	21	1.4	506	61	AA224501	z16f05.r1 Stratagene	9.46e-03
42	21	1.4	506	82	HS1144029	z16f05.r1 Stratagene	9.46e-03
43	21	1.4	589	27	NMAA12293	mu40g03.r1 Soares 2nb	9.46e-03
44	21	1.4	589	22	AA210214	mu40g03.r1 Soares 2nb	9.46e-03
45	21	1.4	1035	95	NM54110	mb68f10.r1 Soares mou	9.46e-03

ALIGNMENTS

RESULT 1 AA233719 463 bp mRNA EST 28-FEB-1997
LOCUS z17908.r1 Soares NIHMPu S1 Homo sapiens CDNA clone 666590 5'
DEFINITION AA233719
ACCESSION g1856711
NID
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; Mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Euthera; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (Bases 1 to 463)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The Washu-Merck EST Project
Unpublished (1995)
TITLE JOURNAL
COMMENT

Contact: Wilson RK
Washu-Merck EST Project
Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Email: estewatson.wustl.edu

This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.jnl.gov) for further information.

Seq primer: -28m13 rev2 ET from Amersham

High quality sequence stop: 448.

FEATURES

Source

1..463

/organism="Homo sapiens"

/note="Organ: mixed (see below); Vector: p7773D-Pac

(Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 2NDHM, pregnant uterus

NbHPU, and fetal heart NBH19W) were mixed, and ss circles

were made in vitro. Following HAP purification, this DNA

was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from pools of

5,000 clones made from the same 3 libraries. The pools

consisted of T.M.A.G.E. clones 260232-265223,

340488-345479, and 484488-489479."

/clone="666590"

/clone_1lb="Soares NhHMPu S1"

/tissue_type="Pooled human melanocyte, fetal heart, and

pregnant uterus"

/lab_host="DH10B"

<1..>463

BASE COUNT 154 a 104 c 88 g 117 t

ORIGIN

Query Match 30.2%; Score 461; DB 65; Length 463;

Best Local Similarity 99.8%; Pred. No. 0.00e+00;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 aggcctgcaaacaccagctgacagatcctgaagctgctcagtttggcgataaaatg 60

995 AGGCATGCAAAACCCAGCTGACGATCCTGAAGCTGCTGTTGGCAATAAAAAAG 1054

61 ggcacccaagacacctggaagggcctaagtcacgcactaaagcactaaagcgtacc 120

1055 GCGACCAAGACACCTGGAAGGGCTATGACGCACTAAGACCTAAGACGTACCACT 1114

121 tcccccaaaccttcaactcagagttcctaagaagacatcaggttctctccacactcaca 180

1115 TTCCCAAAACCTGTCACTCGAGTCTAAAGAACCATCGAGTCTTCACACCTTCACAA 1174

181 tgtacaattgtatcagaagtatttttgaagtataagtaaccaggtccaatcagtaa 240

1175 TGTACAAATGTAATCAGAAATTAATTTTGAAGTATAGTAAACGATCAATCAATTA 1234

241 aataagctgtctataaactggaatgagccatgagctgttctccacaattggcgagatc 300

1235 AATTAAGCTGCTTAATAACGAAATGGCCATGAGCTGTTCTCTCAATTTGGCAGATC 1294

301 ccattgtagagtaaacctgttctcagggcacttgaggtcttcagttatatacttccatca 360

1295 CCATGAGTAGTAACCTGTTTCTCAGGCACTTGAGGCTTCAGTGTATATCTTTCATTA 1354

361 ccagtgactaatattggccacaggtgactaaagaactatgattgaggaagaagagctaac 420

1355 CCAAGTGACTAATTTTGGCCACAGGGAATCTAAAGAACTATGATGTGGAGAAAGGACTAAC 1414

421 atctcctccaataaaccacaatggttaattccaactgtcagat 463

1415 ATCTCCTCCAATAAACCCCAATGTGTAATCCACTGTGAGAT 1457

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

06-MAR-1997 (Rel. 51, last updated, Version 1)

DE zrt47g08.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 666590 5'.

KW EST.

OC Homo sapiens (human)

OC Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;

OC Vertebrata; Eutheria; Primates; Catarrhini; Homidae; Homo.

RN [1]

RP 1-463

RA Hillier L., Clark N., Dubuque T., Elliston K., Hawkins M.,

RA Holman M., Hultman M., Kucaba T., Le M., Lennon G., Marra M.,

RA Parsons J., Rifkin L., Rohlfing T., Soares M., Tan F.,

RA Trevaakis E., Waterston R., Williamson A., Woldmann P., Wilson R.,

RT "The Mashu-Merck EST Project";

RL Unpublished.

CC Contact: Wilson RK WashU-Merck EST Project Washington University

CC School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,

CC MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email:

CC estewatson.wustl.edu This clone is available royalty-free through

CC LNL; contact the IMAGE Consortium (info@image.jnl.gov) for

CC further information. Seq primer: -28m13 rev2 ET from Amersham High

CC quality sequence stop: 448.

Key Location/Qualifiers

source

1..463

/organism="Homo sapiens"

/note="Organ: mixed (see below); Vector: p7773D-Pac

(Pharmacia) with a modified polylinker; Site_1: Not I;

Site_2: Eco RI; Equal amounts of plasmid DNA from three

normalized libraries (melanocyte 2NDHM, pregnant uterus

NbHPU, and fetal heart NBH19W) were mixed, and ss circles

were made in vitro. Following HAP purification, this DNA

was used as tracer in a subtractive hybridization reaction

clones made from the same 3 libraries. The pools consisted

of T.M.A.G.E. clones 260232-265223, 340488-345479, and

484488-489479."

/clone="666590"

/clone_1lb="Soares NhHMPu S1"

/tissue_type="Pooled human melanocyte, fetal heart, and

pregnant uterus"

/lab_host="DH10B"

<1..>463

MRNA

Sequence 463 bp, 154 A, 104 C, 88 G, 117 T, 0 other:

Query Match 30.2%; Score 461; DB 83; Length 463;

Best Local Similarity 99.8%; Pred. No. 0.00e+00;

Matches 463; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 aggcattgcaaacaccagtgacagatcctgaagctgctcagtttggcgataaaatg 60

995 AGGCATGCAAAACCCAGTACGACGATCCTGAAGCTGCTGTTGGCAATAAAAATG 1054

61 ggcacccaagacaccttgaagggcctaagtcacgcactaaagcactaaagcgtacc 120

1055 GCGACCAAGACACCTTGAAGGGCTTAATGACGCACTAAGACCTAAGACGTACCACT 1114

121 tccccaaactgtcactcagaagttcctaagaagacatcaggttctctccacactcaca 180

1115 TTCCCAAAACCTGTCACTCGAGTCTAAAGAACCATCGAGTCTTCACACCTTCACAA 1174

181 tgtcaaatgtatcagaagtatttttgaagtataagtaaccaggtccaatcagtaa 240

1175 TGTCAAAATGTAATCAGAAATTAATTTTGAAGTATAGTAAACGATCAATCAATTA 1234

241 aataagctgtctataaactggaatgagccatgagctgttctccacaattggcgagatc 300

1235 AATTAAGCTGCTTAATAACGAAATGGCCATGAGCTGTTCTCTCAATTTGGCAGATC 1294

301 ccattgtagtaaacctgttctcagggcacttgaggtcttcagttatatacttccatca 360

1295 CCATGAGTAGTAACCTGTTTCTCAGGCACTTGAGGCTTCAGTGTATATCTTTCATTA 1354

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db 361 ccagtgactaatgtccacaggtactaaagaacatagtatgtagaagaagactaac 420
|||||
QY 1355 CCAGTACTAATTTTCCACAGGGTCTAAAGAACTATGATGTGGAGAAAGGACTAAC 1414
|||||
Db 421 atctctccaataaacccaatggttaatccaactgtcagat 463
|||||
QY 1415 ATCTCTCCATAAACCCCAATGTTATCCACACTGCTAGAT 1457
|||||
RESULT 3 AA195113 530 bp mRNA EST 17-JAN-1997
LOCUS zr35a03.r1 Soares NHMPu SI Homo sapiens cDNA clone 665356 5'
DEFINITION AA195113
ACCESSION g1784803
NID g1784803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 530)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
1..530
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/clone="665356"
/clone_lib="Soares NHMPu SI"
/lab_host="DH10B"
/lab_host="DH10B"
MRNA
BASE COUNT 170 a 96 c 93 g 168 t 3 others
ORIGIN
Query Match 21.9%; Score 335; DB 16; Length 530;
Best Local Similarity 97.7%; Pred. No. 0.00e+00;
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 1 acaaatgtatcagaagttatttttagaataatgatagtaccaggtccatcagtaaaaa 60
|||||
QY 1178 ACAAAATGTATCAGAAAGTTATTTTGAATAATGATAGCTAACAGGTCACATCAGTAAAAA 1237
|||||
Db 61 taagctgcttataactggaatgagccatgagctgtttccaccacattgycgagatccca 120
|||||
QY 1238 TAAGCTGTTATTAACGAAATGCGCATGAGCTGTTCTCACAATTCGGCGAGATCCA 1297
|||||
Db 121 tggatagagaactgtttctcaggacctgaggcttcagtgatatactttccatcaca 180
|||||

QY 1298 TGGATGAGTAACGTGTTCTCAGGCACTTAGAGCTTTCAGTGATATCTTCTCATTAACA 1357
|||||
Db 181 gtgactaatlttgcacacaggttactaaagaacatgatgntggaagaagactaacac 240
|||||
QY 1358 GTGACTAATTTTGGCCACAGGGTACTAAAGAACTATGATGTGGAGAAAGGACTAACATC 1417
|||||
Db 241 tctctcaataaacccaatggttaatccaactgtcagatcgtatgtatcttactgtac 300
|||||
QY 1418 TCTTCCAATTAACCCCAATGTTATCACA3CTGCAGATCGTTATCTACTGAC 1477
|||||
Db 301 tataatcccccttatactgcttcgttaattccgactggaatcaaaaa 350
|||||
QY 1478 TATATTTCCCTTATTAATGCTTGCAGTAAATTCAGTGGAAAAA 1527
|||||
RESULT 4 AA195113 530 bp mRNA EST 14-FEB-1997
LOCUS zr35a03.r1 Soares NHMPu SI Homo sapiens cDNA clone 665356 5'.
DEFINITION AA195113
ACCESSION g1784803
NID g1784803
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 530)
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.
The WashU-Merck EST Project
Unpublished (1995)
TITLE
JOURNAL
COMMENT
Contact: Wilson RK
WashU-Merck EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
High quality sequence stop: 257.
Location/Qualifiers
1..530
/organism="Homo sapiens"
/note="Organ: mixed (see below); Vector: pT7T3D-Pac
(Pharmacia) with a modified polylinker; Site_1: Not I;
Site_2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."
/clone="665356"
/clone_lib="Soares NHMPu SI"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
MRNA
BASE COUNT 170 a 96 c 93 g 168 t 3 others
ORIGIN
Query Match 21.9%; Score 335; DB 54; Length 530;
Best Local Similarity 97.7%; Pred. No. 0.00e+00;
Matches 342; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
Db 1 acaaatgtatcagaagttatttttagaataatgatagtaccaggtccatcagtaaaaa 60
|||||

Oy	1178	ACAATTGTGATCAGAAAGTTATTTTANGAANTGATAGTAACCAAGTGCCAAATGATGAATAAA	1237
Db	61	taagctgtcattactggaataatggccattgagtcttccctcaaatggcgagatccca	120
Oy	1238	TAAAGTCCTTATATACGTGAANAAGCGCATGTAGACTCTTTCTTCACAAATGGCGAGATCCCA	1297
Db	121	tggatgaactaaacgtttcttcaggacctgaagccttcaagfatatcttcccatacca	180
Oy	1298	TGGAGAGATGAACACTGTTTTCTCAGGCAGCTTGAGGCTTTGAGTGATATCTTTCCATTACC	1357
Db	181	gtgaactatttgcacacagggtactcaaaaagaacatgatgngagaagaagactaacac	240
Oy	1358	GTCAGCTATTTTTCACACAGGCGTACCTAAAAGAACATATGATGTGGAGAAAGACTAACATC	1417
Db	241	tctccaataaacccccaaatggtatccacaactgtcagatctgtagcttatcactcac	300
Oy	1418	TCTTCACATTAACCCCAATGGTATATCCAACTGCATGCATGTGATCTGATCTACTGAC	1477
Db	301	tatatcttcccattactgctgttggtatcttcgcgctggaattaaaaa	350
	1478	TATATTTTCCCCTTATTACTGCTTGAGATGATTAATCACTGAAAAAATAAA	1527
RESULT	5		
ID	MN1135	standard; RNA; EST; 105 BP.	
AC	W10113;		
N1	g1284430		
DT	29-APR-1996 (Rel. 47, Created)		
DT	05-MAR-1997 (Rel. 51, Last updated, Version 2)		
DE	ma2d03.r1 Soares mouse p3NMf19.5 Mus musculus cDNA clone 313349		
DE	5.		
KW	EST.		
OS	Mus musculus (house mouse)		
OC	Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;		
OC	Vetebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
OC	Mus.		
RN	[1]		
RP	1-105		
RA	Marras M., Hillier L., Allen M., Bowles M., Dietrich N.,		
RA	Dubugue T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,		
RA	Morris M., Schellenberg K., Stepien M., Tan F., Underwood K.,		
RA	Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,		
RA	Waterston R.;		
RT	"The WashU-HMI Mouse EST Project";		
RL	Unpublished.		
CC	Contact: Marra M/Mouse EST Project WashU-HMI Mouse EST Project		
CC	Washington University School of MedicineP 444 Forest Park Parkway,		
CC	Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810		
CC	Email: mouseest@wustl.wustl.edu This clone is available		
CC	royalty-free through LNL ; contact the IMAGE Consortium		
CC	(info@image.llnl.gov) for further information. Putative full length		
CC	read Seq primer: mob.RGA+ET.		
FH	key		
FH	Location/Qualifiers		
FT	source		
FT	1..105		
FT	/organism="Mus musculus"		
FT	/note="Vector: pT73D (Pharmacia) with a modified		
FT	polylinker. Site_1: Not I; Site_2: Eco RI; 1st strand cDNA		
FT	was primed with a Not I - oligo(dt) primer [5',		
FT	TGTTACCAATCTGAAGTGGAGCGCGCCGATTTTTTTTTTTTTTTT 3'] ,		
FT	TGTTACCAATCTGAAGTGGAGCGCGCCGATTTTTTTTTTTTTTTT 3'] ,		
FT	double-stranded cDNA was size selected, ligated to Eco RI		
FT	adapters (Pharmacia), digested with Not I and cloned into		
FT	the Not I and Eco RI sites of a modified pT73 vector		
FT	(Pharmacia). Library went through one round of		
FT	normalization to a Cot = 5. Library constructed by Bento		
FT	Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr		
FT	Minoru Ko (Wayne State University)." .		
FT	/clone="313349"		
FT	/clone_lib="Soares mouse p3NMf19.5"		
FT	/dev_stage="19.5 dpc total fetus"		
FT	/lab_host="DR10B (ampicillin resistant)"		
FT	<1...>105		
FT	MRNA		

SQ	Sequence	105 BP;	57 A; 13 C; 21 G; 14 T; 0 other:
	Query Match	1.4%; Score 21; DB 91; Length 105;	
	Best Local Similarity	76.9%; Pred. No. 9,46e-03;	
	Matches	30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
D8	48	aaagaataatggaaaaaaaagcaaaaaaaaaaacacacaa	86
QY	957	AAAGAAAGTGGACGACAGACATTGAATAAACATATAA	995
RESULT	6	standard: RNA; EST: 107 BP.	
ID	MMA17046	standard: RNA; EST: 107 BP.	
AC	AAL17046;		
NI	91672122		
DT	17-NOV-1996 (Rel. 49, Created)		
DE	18-FEB-1997 (Rel. 51, Last updated, Version 2)		
KW	mp3f02.r1 Soares 2NbMt Mus musculus cDNA clone 572955 5'.		
OS	Eukaryote; mitochondrial eukaryotes; Metazoa; Chordata;		
OC	Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;		
NC	Mus.		
RN	[1]		
RP	1-107		
RA	Maria M., Hillier L., Allen M., Bowles M., Dietrich N.,		
RA	Dubugue T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,		
RA	Morris M., Schellenberg K., Stepien M., Tan F., Underwood K.,		
RA	Moore B., Reising B., Wylie T., Lennon G., Soares B., Wilson R.,		
RA	Waterston R.,		
RT	"The WashU-HMI Mouse EST Project";		
RL	Unpublished.		
CC	Contact: Maria M/Mouse EST Project WashU-HMI Mouse EST Project		
CC	Washington University School of Medicine 444 Forest Park Parkway,		
CC	Box 8801, St. Louis, MO 63108 Tel.: 314 286 1800 Fax: 314 286 1810		
CC	Email: mouseest@wustl.edu This clone is available		
CC	royalty-free through LNL; contact the IMAGE Consortium		
CC	(info@image.lln.gov) for further information. MGI:347603 Putative		
CC	full length rev vector to vector length is 108 Seq primer: -28M13		
CC	rev2 from Amersham.		
FH	Key		
FT	Location/Qualifiers		
FT	source		
FT	1..107		
FT	/organism="Mus musculus"		
FT	/strain="C57BL/6J"		
FT	/note=Vector: pPT3D-Pac (Pharmacia) with a modified		
FT	polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA		
FT	was primed with a Not I - oligo(dT) primer [5'		
FT	TGTACCACATCGACAGCGCGCGCTTTTTCCTTTTTTTTTTTTTTTT		
FT	3']; double-stranded cDNA was ligated to Eco RI adaptors		
FT	(Pharmacia), digested with Not I and cloned into the Not I		
FT	and Eco RI sites of the modified pT713 vector. RNA provide		
FT	d		
FT	by Dr. Bertrand Jordan. Library went through two rounds of		
FT	normalization, and was constructed by Bento Soares and		
FT	M.Fatima Bonaldo."		
FT	/clone="572955"		
FT	/clone_l1b="Soares 2NbMT"		
FT	/sex="male"		
FT	/tissue_type="Thymus"		
FT	/dev_stage="4 weeks"		
FT	/lab_host="DH10B"		
FT	<1..>107		
SO	Sequence 107 BP; 50 A; 16 C; 24 G; 17 T; 0 other:		
	Query Match	1.4%; Score 21; DB 98; Length 107;	
	Best Local Similarity	76.9%; Pred. No. 9,46e-03;	
	Matches	30; Conservative 0; Mismatches 9; Indels 0; Gaps 0;	
D8	65	aaagaataatggaaaaaaaagcaaaaaaaaaaacacacaa	103
QY	957	AAAGAAAGTGGACGACAGACATTGAATAAACATATAA	995

Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TCGTTGACTGTTGTTTATTTGGA
Primer B: AAAGGAGTCAGAAATGGGTTTTT

STS size: 100
PCR Profile:

Presoak:

Denaturation:
Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from random genomic sequence.

Location/Qualifiers

1..245

/organism="Homo sapiens"

56..155

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: CATTGCTTCATACATACAGTTCC
Primer B: CACACTTGAGAGCCGTCGC

STS size: 225
PCR Profile:

Presoak:

Denaturation:
Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from 238433 -- dbEST.

Location/Qualifiers

1..253

/organism="Homo sapiens"

29..253

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TCGTTGACTGTTGTTTATTTGGA
Primer B: AAAGGAGTCAGAAATGGGTTTTT

STS size: 100
PCR Profile:

Presoak:

Denaturation:
Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from random genomic sequence.

Location/Qualifiers

1..245

/organism="Homo sapiens"

56..155

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

9 Cambridge Center, Cambridge MA 02142 USA
Tel: 617 252 1900
Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: CATTGCTTCATACATACAGTTCC
Primer B: CACACTTGAGAGCCGTCGC

STS size: 225
PCR Profile:

Presoak:

Denaturation:
Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from 238433 -- dbEST.

Location/Qualifiers

1..253

/organism="Homo sapiens"

29..253

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

/map="923_H_8; 959_F_5; 441.7 CR from top of Chr17 linkage

group"

Fax: 617 252 1902
Email: thudson@genome.wi.mit.edu

Primer A: TCGTTGACTGTTGTTTATTTGGA
Primer B: AAAGGAGTCAGAAATGGGTTTTT

STS size: 100
PCR Profile:

Presoak:

Denaturation:
Annealing: 56 degrees C

Polymerization:

PCR Cycles: 35

Thermal Cycler:

Protocol:

Template: 10 ng

Primer: each 5 pm

dNTPs: each 4 mM

Taq Polymerase: 0.025 units/ul

Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM

KCl: 50 mM

Tris-HCl: 10 mM

pH: 9.3

Prepared with primer pairs derived from random genomic sequence.

Location/Qualifiers

1..245

/organism="Homo sapiens"

56..155

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963_G_6"

/map="791_B_4; 816_F_6; 921_C_9; 928_A_7; 934_F_6;

963

```

RT      "The WashU-HHMI Mouse EST Project";
RL      Unpublished.
CC      Contact: Maria M/Mouse EST Project WashU-HHMI Mouse EST Project
CC      Washington University School of Medicine 4444 Forest Park Parkway,
CC      Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC      Email: mouseest@wustl.wustl.edu This clone is available
CC      royally-free through LNLN; contact the IMAGE Consortium
CC      (info@image.lnl.gov) for further information. Putative full length
CC      read Seq primer: ETPprimer.
FH      Key      Location/Qualifiers
FH      source      1..267
FH      FT      /organism="Mus musculus"
FH      FT      /note="Vector: pT73D (Pharmacia) with a modified
FH      FT      polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
FH      FT      was primed with a Not I - oligo(dT) primer (5'
FH      FT      TGTTCACATCTGAGTGGAGCGCGCGCATTTTCTTTTCTTTT 3')
FH      FT      double-stranded cDNA was size selected, ligated to Eco RI
FH      FT      adapters (Pharmacia), digested with Not I and cloned into
FH      FT      the Not I and Eco RI sites of a modified pT73 vector
FH      FT      (Pharmacia). Library went through one round of
FH      FT      normalization to a Cot = 5. Library constructed by Bento
FH      FT      Soares and M.Fatima Bonaldo. RNA was kindly provided by Dr
FH      FT      Minoru Ko (Wayne State University)."
FH      FT      /clone_lib="Soares mouse p3NMFL19.5"
FH      FT      /dev_stage="19.5 dpc total fetus"
FH      FT      /lab_host="DH10B (ampicillin resistant)"
FH      FT      <1..>267
FH      FT      mRNA
FH      FT      Sequence 267 BP: 78 A; 70 C; 61 G; 58 T; 0 other;
SQ
Query Match      1.4%; Score 22; DB 95; Length 267;
Best Local Similarity 75.0%; Pred. No. 5.47e-04;
Matches 33; Conservative 0; Mismatches 11; Indels 0; Gaps 0;
Db      31 gaagctcgtggaagcagagagacatctctgcctctgc 74
      ||||| ||||| ||||| ||||| ||||| |||||
CP      931 GAAAGCTGCTCGAAGAGTGAGGTTAGCATGTCCATGTGCCCTGC 888

RESULT 15
ID      MM157384 standard; RNA; EST; 281 BP.
AC      AA239461;
NT      G1863675
DT      06-MAR-1997 (Rel. 51, Created)
DT      15-MAR-1997 (Rel. 51, Last updated, Version 2)
PF      mv25d08.r1 GuayWoodford Beier mouse kidney day 0 Mus musculus cDNA
      clone 656079 5' similar to TR:G497940 G497940 MAJOR VAVLT PROTEIN.
      :
KW      EST.
OS      Mus musculus (house mouse)
OC      Eukaryota; mitochondrial eukaryotes; Metazoa; Chordata;
OC      Vertebrata; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
OC      Mus.
RN      1-281
RP      Maira M., Hillier L., Allen M., Bowles M., Dietrich N.,
RA      Dubuque T., Geisel S., Kucaba T., Lacy M., Le M., Martin J.,
RA      Morris M., Schellenberg K., Steptoe M., Tan F., Underwood K.,
RA      Moore B., Theising B., Wylie T., Lennon G., Soares B., Wilson R.,
RA      Waterston R.,
RT      "The WashU-HHMI Mouse EST Project";
RL      Unpublished.
CC      Contact: Maria M/Mouse EST Project WashU-HHMI Mouse EST Project
CC      Washington University School of Medicine 4444 Forest Park Parkway,
CC      Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810
CC      Email: mouseest@wustl.wustl.edu This clone is available
CC      royally-free through LNLN; contact the IMAGE Consortium
CC      (info@image.lnl.gov) for further information. MGI:401927 Putative
CC      full length vector to vector length is 295 Seq primer: -28m13
CC      rev1 ET from Amerham High quality sequence stop: 272.
FH      Key      Location/Qualifiers

```

```

FH      source      1..281
FH      FT      /organism="Mus musculus"
FH      FT      /strain="C57BL/6J"
FH      FT      /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
FH      FT      XhoI; Cloned unidirectionally. Primer: Oligo dT. Average
FH      FT      insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor
FH      FT      sequence: 5' GAATTCGCGACGAC 3' -3' adaptor sequence: 5'
FH      FT      CTCGAGTTTCTTTTCTTTTCTTTTCTTTT 3' Library provided Lisa
FH      FT      Guay-Woodford."
FH      FT      /clone_lib="GuayWoodford Beier mouse kidney day 0"
FH      FT      /dev_stage="newborn (day 0)"
FH      FT      /lab_host="SOLR (kanamycin resistant)"
FH      FT      <1..>281
FH      FT      mRNA
FH      FT      Sequence 281 BP: 69 A; 75 C; 90 G; 47 T; 0 other;
SQ
Query Match      1.4%; Score 22; DB 92; Length 281;
Best Local Similarity 80.6%; Pred. No. 5.47e-04;
Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Db      148 tgggcccggaaacatcaggagacttgctgtgctg 183
      ||| ||||| ||| ||||| ||||| |||||
CP      43 TGGTCCCGGAAACCTCAGGGGCTTGAGCGCGCG 8

Search completed: Thu Aug 21 10:48:17 1997
Job time : 773 secs.

```